Sequence Search Summary

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2003, 14:40:29 ; Search time 5258 Seconds
                                            (without alignments)
                                            10992.425 Million cell updates/sec

Title: US-09-537-710B-1
Perfect score: 1986
Sequence: 1 atgggcacactgtttcgaag..........agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

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28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1986	100.0	1986	6	AX037577	AX037577 Sequence
	2	1986	100.0	1986	6	AX037595	AX037595 Sequence
	3	1986	100.0	1986	6	AX037597	AX037597 Sequence
	4	1986	100.0	1986	6	AX090382	AX090382 Sequence
	5	1986	100.0	2575	8	SCYNR008W	Z71623 S.cerevisia
	6	1986	100.0	23901	8	SCN201952	X77395 S.cerevisia
	7	273.4	13.8	103568	8	CNS07EGJ	AL590462 DNA centr
	8	202	10.2	2312	6	AX037579	AX037579 Sequence
	9	202	10.2	2312	6	AX037599	AX037599 Sequence
	10	202	10.2	42391	8	SPBC776	AL035263 S.pombe c
	11	117.4	5.9	2013	6	AX090380	AX090380 Sequence
	12	117.4	5.9	2016	6	AX412864	AX412864 Sequence
	13	117.4	5.9	2402	8	AY052715	AY052715 Arabidops
	14	117.4	5.9	2427	6	AX037581	AX037581 Sequence
	15	63.8	3.2	419	6	AX090321	AX090321 Sequence
	16	63.4	3.2	3107	6	AX090317	AX090317 Sequence
	17	63.4	3.2	3685	6	AX037580	AX037580 Sequence
	18	63.4	3.2	3685	6	AX037600	AX037600 Sequence
	19	63.4	3.2	79259	8	AB006704	AB006704 Arabidops
	20	63.4	3.2	90472	8	ATT6I14	AL391710 Arabidops
	21	62	3.1	49890	8	ATF28D10	AL391254 Arabidops
c	22	61.8	3.1	190459	2	AP005419	AP005419 Oryza sat
	23	59.2	3.0	616	6	AX037585	AX037585 Sequence
	24	58.6	3.0	254	6	AX090336	AX090336 Sequence
c	25	55	2.8	7218	6	I66494	I66494 Sequence 14
c	26	54.8	2.8	1680	6	AX090318	AX090318 Sequence
	27	49.4	2.5	1641	6	AX090311	AX090311 Sequence
	28	47.4	2.4	1141	6	AX083744	AX083744 Sequence
	29	46.4	2.3	145524	2	AC016777	AC016777 Homo sapi
c	30	46.2	2.3	171260	9	AC026743	AC026743 Homo sapi
c	31	45	2.3	180995	9	AC117500	AC117500 Homo sapi
	32	45	2.3	187615	2	AC020724	AC020724 Homo sapi
	33	43.8	2.2	324	6	AX090335	AX090335 Sequence

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2003, 14:35:44 ; Search time 479 Seconds
                                          (without alignments)
                                          9337.095 Million cell updates/sec

Title: US-09-537-710B-1
Perfect score: 1986
Sequence: 1 atgggcacactgtttcgaag..........agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_101002:*
                1: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                3: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                5: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                6: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                7: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
                8: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
                9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
                10: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1989.DAT:*
                11: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
                12: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
                13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:*
                14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
                15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
                16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
                17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
                18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
                19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
                20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1986	100.0	1986	21	AAC64431	Saccharomyces cere
	2	1986	100.0	1986	21	AAC64440	Saccharomyces cere
	3	1986	100.0	1986	22	AAS01342	Yeast LCAT related
	4	1958.8	98.6	1986	21	AAC64441	Saccharomyces cere
	5	202	10.2	2312	21	AAC64432	Schizosaccharomyce
	6	202	10.2	2312	21	AAC64442	Schizosaccharomyce
	7	117.4	5.9	2013	22	AAS01341	Arabidopsis thalia
	8	117.4	5.9	2427	21	AAC64434	Arabidopsis thalia
	9	63.8	3.2	419	22	AAS01089	Soybean sterol acy
	10	63.4	3.2	3107	22	AAS01085	Arabidopsis thalia
	11	63.4	3.2	3685	21	AAC64433	Arabidopsis thalia
	12	63.4	3.2	3685	21	AAC64443	Arabidopsis thalia
	13	59.2	3.0	616	21	AAC64436	Neurospora crassa
	14	58.6	3.0	254	22	AAS01104	Corn sterol acyltr
c	15	54.8	2.8	1680	22	AAS01086	Arabidopsis thalia
	16	49.4	2.5	1641	22	AAS01082	Arabidopsis thalia
c	17	44.2	2.2	4590	22	AAH24065	Yeast AOD9604-asso
	18	43.8	2.2	324	22	AAS01103	Corn sterol acyltr
c	19	42.4	2.1	32763	22	AAK68779	Human immune/haema
	20	42	2.1	356	22	AAS01097	Corn sterol acyltr
c	21	41.8	2.1	3642	21	AAA70180	Plasmodium falcipa
	22	41.2	2.1	6271	22	AAS46456	Tumour suppressor
	23	41.2	2.1	6271	24	ABK33978	Human DNA for stag
	24	41.2	2.1	6271	24	ABL33337	Human immune syste
	25	41	2.1	2903	23	ABL15408	Drosophila melanog
	26	41	2.1	5314	24	ABL54309	Chemically treated
	27	41	2.1	5314	24	ABL32160	Human immune syste
	28	40.6	2.0	6327	22	AAS45445	Chemically pretrea
	29	40.6	2.0	6327	24	ABK28294	DNA transcription
	30	40	2.0	5879	24	ABL32269	Human immune syste
	31	40	2.0	7201	24	ABL32337	Human immune syste
	32	39.8	2.0	6298	24	ABL34471	Human metastasis a
	33	39	2.0	3545	22	AAS25965	Human cDNA encodin
	34	39	2.0	4441	21	AAA47759	KIAA0160 cDNA. Ho
	35	39	2.0	4441	24	ABL69961	Pancreas cancer re
	36	38.6	1.9	328	22	AAS01096	Corn sterol acyltr
c	37	38.6	1.9	3082	23	ABL09528	Drosophila melanog
c	38	38.6	1.9	3624	23	ABL16658	Drosophila melanog
c	39	38.6	1.9	23449	21	AAZ35393	Maize amylose-exte
c	40	38.6	1.9	24333	22	AAF75570	Drosophila HDJ1 re
	41	38.4	1.9	674	21	AAF13480	Aspergillus oryzae
	42	38.4	1.9	6109	24	ABL33731	Human immune syste
	43	38.2	1.9	915	20	AAX61750	B. burgdorferi ant
	44	38.2	1.9	975	20	AAX61749	B. burgdorferi ant
	45	38.2	1.9	1183	21	AAC41706	Arabidopsis thalia

OM nucleic - nucleic search, using sw model

Run on: August 1, 2003, 14:42:19 ; Search time 2932 Seconds
                                            (without alignments)
                                            10970.067 Million cell updates/sec

Title: US-09-537-710B-1
Perfect score: 1986
Sequence: 1 atgggcacactgtttcgaag..........agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: gb_gss:*
                 18: em_gss_hum:*
                 19: em_gss_inv:*
                 20: em_gss_pln:*
                 21: em_gss_vrt:*
                 22: em_gss_fun:*
                 23: em_gss_mam:*
                 24: em_gss_mus:*
                 25: em_gss_other:*
                 26: em_gss_pro:*
                 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	439	22.1	832	17	CNS06OAQ	AL407832 T7 end of
c	2	427.8	21.5	948	17	CNS06Y94	AL420734 T3 end of
c	3	324.8	16.4	400	17	AZ924376	AZ924376 4906.ic28
	4	291.6	14.7	978	17	CNS06TH7	AL414545 T7 end of
c	5	249.8	12.6	882	17	CNS07EA9	AL441511 T7 end of
c	6	241.2	12.1	474	17	AZ928292	AZ928292 479.dif06
c	7	194.6	9.8	849	17	CNS06V5M	AL416720 T7 end of
	8	122.6	6.2	605	10	BE450991	BE450991 EST401878
	9	122.2	6.2	719	14	BQ865802	BQ865802 QGC5O21.y
	10	119.8	6.0	821	14	BM780050	BM780050 EST590626
	11	118.2	6.0	854	12	BG645669	BG645669 EST507288
	12	112.8	5.7	634	14	BQ870476	BQ870476 QGD9C14.y
	13	108.8	5.5	586	10	AV940595	AV940595 AV940595
	14	108.8	5.5	610	13	BJ472152	BJ472152 BJ472152
	15	108.8	5.5	628	13	BJ478864	BJ478864 BJ478864
	16	108.8	5.5	674	13	BJ480170	BJ480170 BJ480170
	17	107.2	5.4	724	14	BQ803421	BQ803421 WHE2837_D
	18	104.2	5.2	566	13	BJ470786	BJ470786 BJ470786
	19	95	4.8	575	10	AV938810	AV938810 AV938810
	20	85.8	4.3	631	12	BF053150	BF053150 EST438380
	21	85.6	4.3	626	10	AW587308	AW587308 EST318931
	22	84.8	4.3	477	12	BG313245	BG313245 WHE2051_F
	23	82.4	4.1	337	12	BG888464	BG888464 EST514315
	24	81.4	4.1	420	9	AJ475674	AJ475674 AJ475674
	25	79.8	4.0	525	10	BE204720	BE204720 EST397396
	26	79.6	4.0	874	13	BI951204	BI951204 HVSME1002
	27	79.2	4.0	696	12	BG646723	BG646723 EST508342
	28	78.4	3.9	541	13	BI427198	BI427198 sah77e04.
	29	76.2	3.8	381	13	BI187986	BI187986 b3h11fs.r
	30	71.8	3.6	554	17	AQ942767	AQ942767 Sheared D
	31	70	3.5	560	12	BF053224	BF053224 EST438454
c	32	69.8	3.5	654	14	BQ796112	BQ796112 EST 5050
	33	68.4	3.4	360	9	AJ475673	AJ475673 AJ475673
	34	68.4	3.4	616	10	AV937989	AV937989 AV937989
	35	68	3.4	462	13	BJ482217	BJ482217 BJ482217
	36	67.2	3.4	534	10	AW067535	AW067535 660013G09
	37	62	3.1	595	10	AW649768	AW649768 EST328222
	38	61.6	3.1	493	12	BG369980	BG369980 HVSMEi002
	39	60.6	3.1	482	13	BJ463683	BJ463683 BJ463683
	40	60	3.0	552	13	BI675028	BI675028 949077B06
	41	60	3.0	622	13	BI596075	BI596075 949077B06
	42	60	3.0	1049	12	BG837964	BG837964 Zm10_03f0
c	43	59.8	3.0	474	10	AW334429	AW334429 S34G1 AGS
c	44	59.8	3.0	558	10	AW334432	AW334432 S34G9 AGS
c	45	59.6	3.0	412	13	BI187985	BI187985 b3h11fs.f

ALIGNMENTS

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2003, 14:43:19 ; Search time 102 Seconds
                                             (without alignments)
                                             5971.177 Million cell updates/sec

Title: US-09-537-710B-1
Perfect score: 1986
Sequence: 1 atgggcacactgtttcgaag..........agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	55	2.8	7218	1	US-08-232-463-14	Sequence 14, Appl
c 2	36.6	1.8	612	4	US-09-328-111-138	Sequence 138, App
c 3	36.4	1.8	658	4	US-08-998-416-595	Sequence 595, App
4	35.6	1.8	695	4	US-08-936-165A-171	Sequence 171, App
c 5	35.2	1.8	4982	3	US-08-699-103B-1	Sequence 1, Appli
c 6	35.2	1.8	4982	4	US-09-229-059-1	Sequence 1, Appli
7	34.2	1.7	1603	4	US-09-009-443-11	Sequence 11, Appl
c 8	34.2	1.7	2238	1	US-08-173-436A-4	Sequence 4, Appli
9	34	1.7	1921	4	US-08-682-767-21	Sequence 21, Appl
10	34	1.7	2126	2	US-08-545-745-1	Sequence 1, Appli
11	33.8	1.7	1540	4	US-09-071-035-67	Sequence 67, Appl

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: .   August 1, 2003, 16:20:25 ; Search time 456 Seconds
                                            (without alignments)
                                    . 8984.911 Million cell updates/sec

Title:.   US-09-537-710B-1
Perfect score: 1986
Sequence: 1 atgggcacactgtttcgaag..........agatgcccttcccaatgtaa 1986

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
                 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
                 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq3:*
                 13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	41.6	2.1	1659	11	US-09-938-842A-4435	Sequence 4435, Ap
2	41.6	2.1	2790	11	US-09-938-842A-698	Sequence 698, App
3	41.2	2.1	6271	15	US-10-172-086-36	Sequence 36, Appl
4	40.6	2.0	6327	15	US-10-239-676-152	Sequence 152, App
5	39	2.0	3545	11	US-09-764-864-144	Sequence 144, App
6	39	2.0	4409	11	US-09-874-162A-7	Sequence 7, Appli
7	39	2.0	4441	11	US-09-969-347-169	Sequence 169, App
8	39	2.0	4441	11	US-09-874-162A-4	Sequence 4, Appli
9	37.6	1.9	550	15	US-10-027-632-65239	Sequence 65239, A
10	37.6	1.9	1115	15	US-10-184-644-440	Sequence 440, App
11	37.6	1.9	1115	15	US-10-184-634-440	Sequence 440, App
12	37.2	1.9	603	10	US-09-815-242-6608	Sequence 6608, Ap
13	37.2	1.9	6253	11	US-09-070-927A-160	Sequence 160, App
14	37	1.9	576	15	US-10-027-632-224534	Sequence 224534,
15	37	1.9	576	15	US-10-027-632-224535	Sequence 224535,
16	37	1.9	12968	15	US-10-239-676-202	Sequence 202, App
17	36.8	1.9	842	15	US-10-027-632-173529	Sequence 173529,
c 18	36.8	1.9	22786	11	US-09-764-877-3727	Sequence 3727, Ap
c 19	36.8	1.9	640681	11	US-09-790-988-1	Sequence 1, Appli
c 20	36.6	1.8	612	11	US-09-879-536-138	Sequence 138, App
21	36.6	1.8	640681	11	US-09-790-988-1	Sequence 1, Appli
22	36.4	1.8	2971	10	US-09-815-242-3842	Sequence 3842, Ap
23	36.4	1.8	5136	11	US-09-070-927A-270	Sequence 270, App
c 24	36.2	1.8	720	15	US-10-027-632-152014	Sequence 152014,
c 25	36.2	1.8	720	15	US-10-027-632-152015	Sequence 152015,
c 26	36.2	1.8	720	15	US-10-027-632-152016	Sequence 152016,
27	36.2	1.8	840	15	US-10-027-632-174248	Sequence 174248,
28	35.8	1.8	3576	15	US-10-087-464-39	Sequence 39, Appl
29	35.8	1.8	15832	15	US-10-239-676-106	Sequence 106, App
30	35.6	1.8	583	10	US-09-864-761-20772	Sequence 20772, A
31	35.6	1.8	695	10	US-09-939-980-171	Sequence 171, App
c 32	35.6	1.8	1790	11	US-09-919-497-22	Sequence 22, Appl
c 33	35.6	1.8	1790	15	US-10-225-567A-13	Sequence 13, Appl
34	35.6	1.8	1959	10	US-09-864-761-4012	Sequence 4012, Ap
c 35	35.6	1.8	14462	12	US-09-843-250-9	Sequence 9, Appli
36	35.6	1.8	1830121	15	US-10-329-960-1	Sequence 1, Appli
c 37	35.4	1.8	547	10	US-09-922-217-1037	Sequence 1037, Ap
c 38	35.4	1.8	547	11	US-09-833-263-1037	Sequence 1037, Ap
c 39	35.4	1.8	547	15	US-10-025-380-1037	Sequence 1037, Ap
40	35.4	1.8	1184	14	US-10-146-731-394	Sequence 394, App
41	35.4	1.8	1184	15	US-10-123-155-394	Sequence 394, App
42	35.4	1.8	14147	15	US-10-172-086-51	Sequence 51, Appl
43	35.4	1.8	20467	11	US-09-764-877-2725	Sequence 2725, Ap
44	35.4	1.8	20467	11	US-09-764-877-2726	Sequence 2726, Ap
c 45	35.4	1.8	22073	12	US-09-764-891-7351	Sequence 7351, Ap

ALIGNMENTS

RESULT 1
US-09-938-842A-4435/c